

opposed to any of the teaching of the cited art, the presently described invention is designed to work within a single species as opposed to the cross-species aspects of the cited references (the present invention does not look for new repeats by comparison to known repeats from other organisms as is taught by the cited references).

Therefore, as the cited art clearly teaches away from the present invention, and as the cited art fails to teach at least one of the key inventive points of the present invention which failure is not cured by or made obvious over any of the secondary references, Applicant respectfully requests removal of this basis of rejection.

Status of the Claims

What is claimed is:

2. (Original). A method for constructing a repeat database comprising:
 - selecting a query sequence;
 - selecting known repeat sequences;
 - adding known repeat sequences into a repeat sequence database;
 - masking said query sequence with repeat sequences in the repeat sequence database;
 - testing said masked query sequence with a redundant file;
 - identifying sequences in the redundant file that contain a similar sequence to a portion of the query sequence, wherein said identified sequences and said similar portion of the query sequence make up a pairwise sequence alignment;
 - aligning all the identified pairwise sequence alignments;

designating the right and left endpoints of each identified sequence and any intervening sequences;

identifying a position within the query sequence corresponding to each endpoint;

defining regions within the query sequence, wherein a region is a sequence between two consecutive positions matching two endpoints;

identifying any two successive regions having a large variance in the number of sequence matches; and

adding the sequence within the region of the two successive regions having the highest number of sequence matches into the repeat sequence database.

3. (Original). The method of claim 2, wherein the large variance in the number of sequence matches is equal to 5 or more.

5. (Currently Amended) The method of claim 2, wherein said query sequence is a deoxyribonucleotide sequence.

6. (Currently Amended) The method of claim 2, wherein said query sequence is a ribonucleotide sequence.

7. (Currently Amended) The method of claim 2, wherein said query sequences are derived from animal DNA or RNA.

8. (Original). The method of claim 7, wherein said animal is a human.

9. (Original). The method of claim 8, wherein said animal is a mouse.
10. (Cancelled).
11. (Cancelled).
12. (Cancelled).
13. (Cancelled).
14. (Cancelled).
15. (Cancelled).
16. (Currently Amended). The method of claim 2, wherein said repeat sequences are postulated based upon amino acid sequences.
17. (Cancelled).
18. (Original). The method of claim 2, wherein said database is encoded in a written medium.
19. (Original). The method of claim 2, wherein said database is encoded in an electronic

medium.

20. (Original). The method of claim 19, wherein said electronic medium is a computer-readable medium.

21. (Original). The method of claim 20, wherein said computer-readable medium is addressable through an internet connection.

22. (Original). The method of claim 2, wherein said redundant file is a Public Domain Database.

23. (Original). The method of claim 22, wherein said Public Domain Database is GenBank.

24. (Original). The method of claim 22, wherein said Public Domain Database is dbEST.

25. (Original). The method of claim 22, wherein said Public Domain Database is TIGR.

26. (Original). The method of claim 22, wherein said Public Domain Database is SwissProt.

27. (Original). The method of claim 2, wherein sequence comparisons are carried out using a Database Search Algorithm.

28. (Original). The method of claim 27, wherein said Database Search Algorithm is BLAST.

29. (Original). The method of claim 27, wherein said Database Search Algorithm is FASTA.
30. (Original). The method of claim 27, wherein said Database Search Algorithm is Smith-Waterman.
31. (Original). The method of claim 2, wherein said sequence comparisons are carried out utilizing a Scoring Matrix Program.
32. (Original). The method of claim 31, wherein said Scoring Matrix Program is PAM.
33. (Original). The method of claim 31, wherein said Scoring Matrix Program is BLOSUM.
39. (Original). An improved database of nucleotide sequences, the improvement consisting of repeat sequences containing a similar sequence to a portion of a query sequence, wherein said identified sequences and said similar portion of the query sequence make up a pairwise sequence alignment, and wherein all identified pairwise sequence alignments have right and left endpoints of each identified sequence and any intervening sequences.

All bases for rejection of the claims has been fully addressed and overcome. Applicants respectfully request that the case be allowed.

The Commissioner is authorized to charge to McDaniel & Associates P.C. Deposit Account No. 50/1085, any fee for extension of time deemed necessary to make timely the filing of this response.

Respectfully submitted,



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